#3

$D_{m}J$

BATCH

2-12-0,

RAW SEQUENCE LISTING   DATE: 02/14/2001
PATENT APPLICATION: US/09/688,286   TIME: 10:31:01

Input Set : A:\688286.txt
Output Set: N:\CRF3\02142001\I688286.raw

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 4 <110> APPLICANT: Willson, Tracy
 5       Nicola, Nicos A.
 6       Hilton, Douglas J.
 7       Metcalf, Donald
 8       Zhang, Jian G.
10 <120> TITLE OF INVENTION: NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES
11       ENCODING SAME
13 <130> FILE REFERENCE: Davies cc
15 <140> CURRENT APPLICATION NUMBER: US/09/688,286
16 <141> CURRENT FILING DATE: 2000-10-13
18 <150> PRIOR APPLICATION NUMBER: 09/051,843
19 <151> PRIOR FILING DATE: 1998-06-29
21 <160> NUMBER OF SEQ ID NOS: 8
23 <170> SOFTWARE: PatentIn Ver. 2.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1383
27 <212> TYPE: DNA
28 <213> ORGANISM: nuc. & predicted a.a. seq. of mNR4
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (61)..(1338)
34 <220> FEATURE:
35 <221> NAME/KEY: unsure
36 <222> LOCATION: (121)
37 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
38       region
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41 <221> NAME/KEY: unsure
42 <222> LOCATION: (122)
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52 <220> FEATURE:
53 <221> NAME/KEY: unsure
54 <222> LOCATION: (640)
55 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
56       region
58 <220> FEATURE:
59 <221> NAME/KEY: unsure
60 <222> LOCATION: (641)
61 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
62       region
64 <220> FEATURE:
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                   RAW SEQUENCE LISTING          DATE: 02/14/2001
                   PATENT APPLICATION: US/09/688,286     TIME: 10:31:01

                   Input Set : A:\688286.txt
                   Output Set: N:\CRF3\02142001\I688286.raw

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  66 <222> LOCATION: (642)
  67 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
  68       region
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  74 atg gcg cgg cca gcg ctg ctg ggc gag ctg ttg gtg ctg cta ctg tgg   108
  75 Met Ala Arg Pro Ala Leu Leu Gly Glu Leu Leu Val Leu Leu Leu Trp
  76  1               5                   10                  15
W-->78 acc gcc acc gtg nnn ggc caa gtt gcc gcg gcc aca gaa gtt cag cca   156
W-->79 Thr Ala Thr Val Xaa Gly Gln Val Ala Ala Ala Thr Glu Val Gln Pro
  80                  20                  25                  30
  82 cct gtg acg aat ttg agc gtc tct gtc gaa aat ctc tgc acg ata ata   204
  83 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile
  84          35                  40                  45
  86 tgg acg tgg agt cct cct gaa gga gcc agt cca aat tgc act ctc aga   252
  87 Trp Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg
  88      50                  55                  60
  90 tat ttt agt cac ttt gat gac caa cag gat aag aaa att gct cca gaa   300
  91 Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu
  92  65                  70                  75                  80
  94 act cat cgt aaa gag gaa tta ccc ctg gat gag aaa atc tgt ctg cag   348
  95 Thr His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln
  96                  85                  90                  95
  98 gtg ggc tct cag tgt agt gcc aat gaa agt gag aag cct agc cct ttg   396
  99 Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu
 100                  100                 105                 110
 102 gtg aaa aag tgc atc tca ccc cct gaa ggt gat cct gag tcc gct gtg   444
 103 Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
 104              115                 120                 125
 106 act gag ctc aag tgc att tgg cat aac ctg agc tat atg aag tgt tcc   492
 107 Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
 108          130                 135                 140
 110 tgg ctc cct gga agg aat aca agc cct gac aca cac tat act ctg tac   540
 111 Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr
 112 145                 150                 155                 160
 114 tat tgg tac agc agc ctg gag aaa agt cgt caa tgt gaa aac atc tat   588
 115 Tyr Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr
 116                  165                 170                 175
 118 aga gaa ggt caa cac att gct tgt tcc ttt aaa ttg act aaa gtg gaa   636
 119 Arg Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu
 120                  180                 185                 190
W-->122 cct nnn agt ttt gaa cat cag aac gtt caa ata atg gtc aag gat aat   684
W-->123 Pro Xaa Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn
 124              195                 200                 205
 126 gct ggg aaa att agg cca tcc tgc aaa ata gtg tct tta act tcc tat   732
 127 Ala Gly Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr
 128          210                 215                 220
 130 gtg aaa cct gat cct cca cat att aaa cat ctt ctc ctc aaa aat ggt   780
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RAW SEQUENCE LISTING                  DATE: 02/14/2001
PATENT APPLICATION: US/09/688,286     TIME: 10:31:01

         Input Set : A:\688286.txt
         Output Set: N:\CRF3\02142001\I688286.raw

131 Val Lys Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly
132 225             230             235             240
134 gcc tta tta gtg cag tgg aag aat cca caa aat ttt aga agc aga tgc   828
135 Ala Leu Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys
136             245             250             255
138 tta act tat gaa gtg gag gtc aat aat act caa acc gac cga cat aat   876
139 Leu Thr Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn
140             260             265             270
142 att tta gag gtt gaa gag gac aaa tgc cag aat tcc gaa tct gat aga   924
143 Ile Leu Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg
144         275             280             285
146 aac atg gag ggt aca agt tgt ttc caa ctc cct ggt gtt ctt gcc gac   972
147 Asn Met Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp
148     290             295             300
150 gct gtc tac aca gtc aga gta aga gtc aaa aca aac aag tta tgc ttt   1020
151 Ala Val Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe
152 305             310             315             320
154 gat gac aac aaa ctg tgg agt gat tgg agt gaa gca cag agt ata ggt   1068
155 Asp Asp Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly
156             325             330             335
158 aag gag caa aac tcc acc ttc tac acc acc atg tta ctc acc att cca   1116
159 Lys Glu Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro
160             340             345             350
162 gtc ttt gtc gca gtg gca gtc ata atc ctc ctt ttt tac ctg aaa agg   1164
163 Val Phe Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg
164     355             360             365
166 ctt aag atc att ata ttt cct cca att cct gat cct ggc aag att ttt   1212
167 Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
168     370             375             380
170 aaa gaa atg ttt gga gac cag aat gat gat acc ctg cac tgg aag aag   1260
171 Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
172 385             390             395             400
174 tat gac atc tat gag aaa caa tcc aaa gaa gaa acg gat tct gta gtg   1308
175 Tyr Asp Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val
176             405             410             415
178 ctg ata gaa aac ctg aag aaa gca gct cct tgatggggag aagtgatttc     1358
179 Leu Ile Glu Asn Leu Lys Lys Ala Ala Pro
180             420             425
182 tttcttgcct tcaatgtgac cctgt                                       1383
186 <210> SEQ ID NO: 2
187 <211> LENGTH: 426
188 <212> TYPE: PRT
189 <213> ORGANISM: nuc. & predicted a.a. seq. of mNR4
191 <220> FEATURE:
192 <221> NAME/KEY: unsure
193 <222> LOCATION: (21)
194 <223> OTHER INFORMATION: authors are unsure about the sequence assignment
196 <220> FEATURE:
197 <221> NAME/KEY: unsure
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    198 <222> LOCATION: (194)
    199 <223> OTHER INFORMATION: authors are unsure about the sequence assignment
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    203  1               5                  10                  15
W--> 205 Thr Ala Thr Val Xaa Gly Gln Val Ala Ala Ala Thr Glu Val Gln Pro
    206             20                  25                  30
    208 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile
    209             35                  40                  45
    211 Trp Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg
    212     50                  55                  60
    214 Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu
    215  65                  70                  75                  80
    217 Thr His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln
    218             85                  90                  95
    220 Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu
    221             100                 105                 110
    223 Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
    224             115                 120                 125
    226 Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
    227     130                 135                 140
    229 Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr
    230 145                 150                 155                 160
    232 Tyr Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr
    233             165                 170                 175
    235 Arg Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu
    236             180                 185                 190
W--> 238 Pro Xaa Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn
    239     195                 200                 205
    241 Ala Gly Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr
    242     210                 215                 220
    244 Val Lys Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly
    245 225                 230                 235                 240
    247 Ala Leu Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys
    248             245                 250                 255
    250 Leu Thr Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn
    251             260                 265                 270
    253 Ile Leu Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg
    254     275                 280                 285
    256 Asn Met Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp
    257     290                 295                 300
    259 Ala Val Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe
    260 305                 310                 315                 320
    262 Asp Asp Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly
    263             325                 330                 335
    265 Lys Glu Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro
    266             340                 345                 350
    268 Val Phe Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg
    269             355                 360                 365
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                RAW SEQUENCE LISTING            DATE: 02/14/2001
                PATENT APPLICATION: US/09/688,286   TIME: 10:31:01

                Input Set : A:\688286.txt
                Output Set: N:\CRF3\02142001\I688286.raw

271 Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
272        370             375             380
274 Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
275 385             390             395             400
277 Tyr Asp Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val
278 ·           405             410             415
280 Leu Ile Glu Asn Leu Lys Lys Ala Ala Pro
281        420             425
284 <210> SEQ ID NO: 3
285 <211> LENGTH: 1383
286 <212> TYPE: DNA
287 <213> ORGANISM: IL-13 receptor alpha-chain
289 <220> FEATURE:
290 <221> NAME/KEY: CDS
291 <222> LOCATION: (61)..(1338)
293 <400> SEQUENCE: 3
294 gagtctaaca cggaccaagg agtttaacac gtgcggccgg gttccgaggc gagaggctgc 60
297 atg gag tgg ccg gcg cgg ctc tgc ggg ctg tgg gcg ctg ctg ctc tgc 108
298 Met Glu Trp Pro Ala Arg Leu Cys Gly Leu Trp Ala Leu Leu Leu Cys
299   1               5                   10                  15
301 gcc ggc ggc ggg ggc ggg ggc ggg ggc gcg cct acg gaa act cag cca 156
302 Ala Gly Gly Gly Gly Gly Gly Gly Gly Ala Pro Thr Glu Thr Gln Pro
303             20                  25                  30
305 cct gtg aca aat ttg agt gtc tct gtt gaa aac ctc tgc aca gta ata 204
306 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile
307         35                  40                  45
309 tgg aca tgg aat cca ccc gag gga gcc agc tca aat tgt agt cta tgg 252
310 Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp
311     50                  55                  60
313 tat ttt agt cat ttt ggc gac aaa caa gat aag aaa ata gct ccg gaa 300
314 Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu
315 65                  70                  75                  80
317 act cgt cgt tca ata gaa gta ccc ctg aat gag agg att tgt ctg caa 348
318 Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln
319                 85                  90                  95
321 gtg ggg tcc cag tgt agc acc aat gag agt gag aag cct agc att ttg 396
322 Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu
323             100                 105                 110
325 gtt gaa aaa tgc atc tca ccc cca gaa ggt gat cct gag tct gct gtg 444
326 Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
327         115                 120                 125
329 act gaa ctt caa tgc att tgg cac aac ctg agc tac atg aag tgt tct 492
330 Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
331     130                 135                 140
333 tgg ctc cct gga agg aat acc agt ccc gac act aac tat act ctc tac 540
334 Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr
335 145             150                 155                 160
337 tat tgg cac aga agc ctg gaa aaa att cat caa tgt gaa aac atc ttt 588
338 Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe
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VERIFICATION SUMMARY   DATE: 02/14/2001
PATENT APPLICATION: US/09/688,286   TIME: 10:31:02

Input Set : A:\688286.txt
Output Set: N:\CRF3\02142001\I688286.raw

L:78 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:79 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:123 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:205 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:238 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2